

Amendments to the Claims

Claim 1 (Currently amended): A method of identifying pigs to determine those with desired meat quality characteristics, comprising: variation in a genotype of an animal, wherein said variation is associated with a phenotypic difference in meat quality traits of said animal, wherein said variation is a polymorphism characterized by an asparagine codon at an amino acid position analogous to amino acid 298 of a human MC4R gene product, wherein said animal with an asparagine codon at position 298 is indicative of said animal more likely to have favorable meat quality characteristics than an animal with an aspartic acid codon at position 298, said method comprising:

obtaining a nucleic acid sample from said ~~animal~~ pigs;

assaying for the presence of a polymorphism in a MC4R gene as set forth in SEQ ID NO:1, of

~~said sample~~ wherein said polymorphism at the amino acid level is characterized as a

change from an aspartic acid codon to an asparagine codon at an amino acid position

corresponding to amino acid 298 of a human MC4R gene product, ~~wherein said animal~~

~~with an asparagine codon is indicative of said animal more likely to have favorable meat~~

~~quality characteristics such as~~ said polymorphism being associated with meat quality

characteristics of pH, color, and drip loss; and pH,

~~marbling, color and drip loss than an animal with an aspartic acid codon at position 298; and~~

relating said polymorphism to said phenotype.

Claims 2-4 (Cancelled).

Claim 5 (Previously presented): The method of claim 1 wherein the step of assaying for the presence of the polymorphism is a method employing allele specific oligonucleotides.

Claim 6 (Previously presented): The method of claim 1 wherein said polymorphism is assayed by PCR amplification and restriction.

Claim 7 (Previously presented): The method of claim 1 wherein the step of assaying for the presence of the polymorphism employs a technique selected from the group consisting of

restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), temperature gradient gel electrophoresis (TGGE), and use of linked genetic markers.

Claim 8 (Previously presented): The method of claim 7 wherein a step of assaying identifying the polymorphism comprises RFLP analysis.

Claim 9 (Previously presented): The method of claim 1 further comprising the step of: amplifying a region of the MC4R gene sequence or a region therein which contains said polymorphism.

Claim 10 (Previously presented): The method of claim 9 further comprising the step of digesting the amplified region with a restriction endonuclease *Taq I*.

Claims 11-18 (Cancelled).

Claim 19 (Previously presented): The method of claim 9 wherein polymorphism is at position 678 of the amplification product produced by primers SEQ ID NO:5 and SEQ ID NO:6.

Claim 20 (Currently amended): A method of identifying ~~an animal~~ pigs which possess a desired genotype indicative of a phenotypic trait, the method comprising:
obtaining a nucleic acid sample from an animal, said sample comprising ~~a seventh transmembrane region of an MC4R gene as set forth in SEQ ID NO:1~~, and
identifying the presence or absence of a *Taq I* site in one allele resulting from a nucleotide substitution at position 678 of the MC4R gene as set forth in SEQ ID NO:1,
wherein the presence of a *Taq I* site indicates that the animal possesses a desired genotype indicative of a phenotypic trait selected from the group consisting of pH, ~~marbling~~, color and drip loss.

Claim 21 (Previously presented): The method of claim 20 further comprising the step of selecting animals with the desired genotype for breeding.

Claim 22 (Currently amended): The method of claim 20 further comprising:
amplifying the nucleic acid sample with a forward primer SEQ ID NO:5 and a reverse primer SEQ ID NO:6;
digesting the amplified nucleic acid with a restriction enzyme such that nucleic acid fragments are generated;
separating the nucleic acid fragments according to size such that a restriction fragment pattern is generated wherein the polymorphism is identifiable by a *Taq I* digestion pattern of an amplified product characterized by fragments of 466, 225, and 76 bp when a guanine is present at base 678 of the MC4R gene and fragments 542 and 225 bp when an adenine is present at base 678 of the amplified product.

Claim 23 (Currently amended): The method of claim ~~22 wherein the restriction fragment pattern is characterized~~ 20 further comprising:
amplifying the nucleic acid sample with a forward primer SEQ ID NO:9 and a reverse primer SEQ ID NO:10;
digesting the amplified nucleic acid with a restriction enzyme such that nucleic acid fragments are generated;
separating the nucleic acid fragments according to size such that a restriction fragment pattern is generated wherein the polymorphism is identifiable by a *Taq I* digestion pattern of an amplified product characterization by fragments of 156 and 70 bp when allele 1 of the MC4R gene is present and a fragment of 226 bp when allele 2 of the MC4R gene is present, when a restriction enzyme that acts at the same recognition site as *Taq I* is used.

Claim 24 (Cancelled).

Claim 25 (Withdrawn): A kit for evaluating a nucleic acid sample from an animal comprising:

a reagent in a container that identifies a polymorphism in a MC4R gene.

Claim 26 (Withdrawn): The kit of claim 25 wherein the reagent is a primer that amplifies the MC4R gene or a fragment thereof.

Claim 27 (Withdrawn): The kit of claim 25 further comprising:
a DNA polymerase which cleaves the MC4R gene,
a forward primer, and
a reverse primer,
wherein the primers are capable of amplifying a region of the MC4R gene which contains a polymorphic site.

Claim 28 (Withdrawn): A primer for assaying the presence of a polymorphic Taq I site in the MC4R gene wherein the primer comprises a sequence selected from the group consisting of SEQ. ID NO:6, SEQ. ID NO:7, SEQ. ID NO:8, SEQ. ID NO:9, SEQ. ID NO:10, and SEQ. ID NO:11.

Claim 29 (Currently amended): A method for selecting ~~animals-pigs~~ for the desired traits of favorable meat quality comprising the steps of:
obtaining a nucleic acid sample from ~~an animal~~ a pig,
identifying a polymorphism said polymorphism being a nucleotide substitution at position 678 of SEQ ID NO:1, and
selecting the ~~animals-pigs~~ which have the nucleotide associated with a desired trait selected from the group consisting of pH, ~~marbling~~, color and drip loss at position 678, wherein the presence of the polymorphism indicates that the ~~animal-pig~~ possesses a genotype
indicative of a favorable meat quality selected from the group consisting of pH, ~~marbling~~, color, and drip loss.

Claim 30 (Currently amended): A method for indirect selection for a polymorphism in an MC4R gene comprising:

obtaining a nucleic acid sample from ~~an animal~~ a pig, and
identifying a nucleotide substitution at position 678 of SEQ ID NO:1 with a DNA marker known to be associated with MC4R gene, said DNA marker further being associated with meat quality characteristics of pH, color and drip loss, wherein specific alleles of the DNA marker are used to make the indirect identification of the nucleotide substitution, and
selecting said ~~animals~~ pigs based upon the presence of nucleotide substitution.

Claim 31 (Original): The method of claim 30 wherein the linked marker is selected from the group consisting of S0331, BHT0433, and S0313.

Claim 32 (Currently amended): A method of identifying ~~animals~~ pigs which possess a desired genotype indicative of favorable meat quality traits, the method comprising:
determining an association between a MC4R genotype and a trait of interest by obtaining a sample of ~~animals~~ pigs from a line or breed of interest,
preparing a nucleic acid sample from each ~~animal~~ pig in the sample,
determining the genotype of the MC4R gene by screening for a polymorphism being a ~~point mutation in the 7th transmembrane domain~~ nucleotide substitution at position 678 of the MC4R gene as set forth in SEQ ID NO:1, wherein the presence of the polymorphism indicates that the animal possesses a genotype indicative of favorable meat quality characteristics selected from the group consisting of pH, ~~marbling~~, color, and drip loss
and
calculating the association between the MC4R genotype and the trait.

Claim 33 (Previously presented): A method of selecting ~~animals~~ pigs which possess a desired MC4R genotype indicative of a ~~significantly associated phenotypic~~ meat quality trait of pH, color, and drip loss, the method comprising:
obtaining a nucleic acid sample from ~~an animal~~ a pig by screening for a polymorphism being a G to A point mutation at position 678 of SEQ ID NO:1 from

the MC4R gene,

identifying the genotype of the MC4R gene of the ~~animal~~ pig, and
selecting those ~~animals~~ pigs which have the genotype associated with the desired traits,
wherein the presence of the polymorphism indicates that the ~~animal~~ pig possesses a genotype
previously shown to be significantly associated with said ~~desired~~ meat quality trait of pH,
color, and drip loss.

Claim 34 (Currently amended): A method of determining the potential meat quality of ~~an~~
~~animal~~ a pig, said method comprising:

obtaining a nucleic acid sample from said ~~animal~~ pig and then assaying for the presence of a
polymorphism in the MC4R gene of the sample, said polymorphism being a G to A point
mutation at position 678 of SEQ ID NO: 1 from the MC4R gene, said polymorphism
being one which is associated with favorable meat quality characteristics selected from
the group consisting of pH, ~~marbling~~, color, and drip loss,
wherein the presence of the polymorphism indicates that the ~~animal~~ pig possesses
a genotype indicative of favorable meat quality.

Claim 35 (Currently amended): A method of selecting ~~animals~~ pigs for breeding, said
method comprising:

obtaining a nucleic acid sample from said ~~animal~~ pig;
assaying for the presence of a polymorphism in the MC4R gene of said sample, said
polymorphism being a G to A point mutation at position 678 of SEQ ID NO:1 from the
MC4R gene, said polymorphism being correlated with a ~~phenotypic~~ meat quality trait of
pH, color, and drip loss; and

using the MC4R genotype as part of a selection model based on the estimated value of the effect
of the marker genotype, and thereafter
selecting ~~animals~~ pigs on the basis of this estimated value for use in breeding.

Claim 36 (Currently amended): A method of segregating ~~animals-pigs~~ in order to provide uniformity at slaughter comprising:
obtaining a nucleic acid sample from said ~~animal~~pig; and
assaying for the presence of a polymorphism in the MC4R gene of said sample, said polymorphism being a G to A point mutation at position 678 of SEQ ID NO:1 from the MC4R gene, said polymorphism being one which is associated with meat quality traits of pH, color, and drip loss,
segregating said ~~animals-pigs~~ based upon the polymorphism present in said animal.

Claim 37 (Currently amended): A method for selecting ~~animals-pigs~~ for breeding, said method comprising:
obtaining a nucleic acid sample from said ~~animal~~pig;
assaying for the presence of a polymorphism ~~in the seventh transmembrane domain~~ of the MC4R gene of said sample said polymorphism being ~~one which~~ a nucleotide substitution at position 678 of SEQ ID NO: 1, and wherein said polymorphism is associated with a phenotypic meat quality trait of pH, color, and drip loss; and
selecting ~~animals-pigs~~ with a favorable allele for inclusion in breeding stock.

Claims 38-39 (Cancelled)

Claim 40 (Currently amended): A method for selecting pigs for the desired trait of improved meat quality comprising the steps of:
obtaining a nucleic acid sample from a pig,
screening said pig for a polymorphism comprising a G to A point mutation at position ~~analogous to position~~ 678 of SEQ ID NO:1 from the MC4R gene, said polymorphism being one which is associated with a favorable meat quality characteristic of pH, color, and drip loss, and
selecting said pig which have the nucleotide associated with the desired traits at position 678.